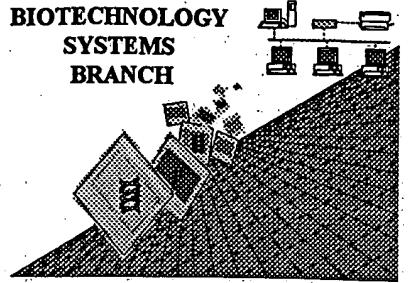


Friedman

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



# RAW SEQUENCE LISTING

## ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/129,958

Art Unit / Team No.: 1605

Date Processed by STIC: 7/20/99

**THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.**

**PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:**

**1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,**

**2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY**

**THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.**

**IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:**

**MARK SPENCER 703-308-4212**

# Raw Sequence Listing Error Summary

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**ERROR DETECTED**   **SUGGESTED CORRECTION**
**SERIAL NUMBER:** 09/129,958

**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE**

- 1  Wrapped Nucleic The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2  Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3  Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4  Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5  Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6  Variable Length Sequence(s)  contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7  PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.
- 8  Skipped Sequences (OLD RULES) Sequence(s)  missing. If intentional, please use the following format for each skipped sequence:  
**(2) INFORMATION FOR SEQ ID NO:X:**  
**(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")**  
**(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:**  
**This sequence is intentionally skipped**  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9  Skipped Sequences (NEW RULES) Sequence(s)  missing. If intentional, please use the following format for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 10  Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11  Use of <213>Organism (NEW RULES) Sequence(s)  are missing this mandatory field or its response.
- 12  Use of <220>Feature (NEW RULES) Sequence(s)  are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13  PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

PAGE: 1

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/129,958DATE: 07/20/1999  
TIME: 16:36:07

Input Set: I129958.RAW

This Raw Listing contains the General Information  
Section and up to first 5 pages.

Does Not Comply  
Corrected Diskette Needed

1 <110> APPLICANT: Mills, Allen P.  
 2 Yurke, Bernard  
 3 Platzman, Philip M.  
 4 <120> TITLE OF INVENTION: ANALOG AND NEURAL NETWORK COMPUTATION USING DNA  
 5 <130> FILE REFERENCE: LUTEC 0008  
 6 <140> CURRENT APPLICATION NUMBER: US/09/129,958  
 7 <141> CURRENT FILING DATE: 1998-08-06  
 8 <150> EARLIER APPLICATION NUMBER: 09/078,761  
 9 <151> EARLIER FILING DATE: 1998-05-15  
 10 <150> EARLIER APPLICATION NUMBER: 09/018,248  
 11 <151> EARLIER FILING DATE: 1998-02-03  
 12 <150> EARLIER APPLICATION NUMBER: 60/086,654  
 13 <151> EARLIER FILING DATE: 1998-05-26  
 14 <160> NUMBER OF SEQ ID NOS: 4  
 15 <170> SOFTWARE: PatentIn Ver. 2.0  
 16 <210> SEQ ID NO 1  
 17 <211> LENGTH: 10  
 18 <212> TYPE: DNA  
 19 <213> ORGANISM: Artificial Sequence  
 20 <220> FEATURE:  
 21 <223> OTHER INFORMATION: Description of Artificial Sequence: DNA based  
 analog oligonucleotide  
 23 <400> SEQUENCE: 1  
 24 agctatcgat  
 25 <210> SEQ ID NO 2  
 26 <211> LENGTH: 34  
 27 <212> TYPE: DNA  
 28 <213> ORGANISM: Artificial Sequence  
 29 <220> FEATURE:  
 30 <223> OTHER INFORMATION: Description of Artificial Sequence: DNA based  
 analog oligonucleotide  
 32 <220> FEATURE:  
 33 <221> NAME/KEY: variation  
 34 <222> LOCATION: (34)  
 35 <400> SEQUENCE: 2  
 36 aatgcaagat cggaaatttat acgtttatct tach ( )  
 37 <210> SEQ ID NO 3  
 38 <211> LENGTH: 34  
 39 <212> TYPE: DNA  
 40 <213> ORGANISM: Artificial Sequence  
 41 <220> FEATURE:  
 42 <223> OTHER INFORMATION: Description of Artificial Sequence: DNA based  
 analog oligonucleotide  
 43 <220> FEATURE:

10

34

*an explanation of "n" is mandatory  
in <223> response  
(see item 10 on  
Euro Summary Sheet)  
and see 1.823 of sequence  
Rules)*

W--&gt;

PAGE: 2

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/129,958DATE: 07/20/1999  
TIME: 16:36:07

Input Set: I129958.RAW

45 <221> NAME/KEY: variation  
46 <222> LOCATION: (34) *same error*  
47 <400> SEQUENCE: 3  
W--> 48 aatgcaagat cgaaatttat acgttatct ta<sup>n</sup> 34  
49 <210> SEQ ID NO 4  
50 <211> LENGTH: 30  
51 <212> TYPE: DNA  
52 <213> ORGANISM: Artificial Sequence  
53 <220> FEATURE:  
54 <223> OTHER INFORMATION: Description of Artificial Sequence: DNA based  
analog oligonucleotide  
56 <400> SEQUENCE: 4  
57 aatgcaagat cgaaatttat acgttatct 30

PAGE: 3

VERIFICATION SUMMARY  
PATENT APPLICATION US/09/129,958

DATE: 07/20/1999  
TIME: 16:36:07

Input Set: I129958.RAW

Line ? Error/Warning

Original Text

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36 W "N" or "Xaa" used: Feature required      aatgcaagat cgaaatttat acgttatct tacn  
48 W "N" or "Xaa" used: Feature required      aatgcaagat cgaaatttat acgttatct tacn